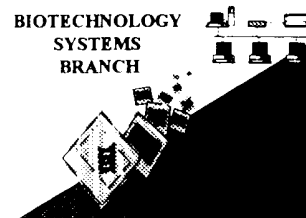


Minutal

RAW SEQUENCE LISTING **ERROR REPORT**



#7

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/004,395
Art Unit / Team No.: 1643
Date Processed by STIC: 1/15/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

PATENT APPLICATION US/09/004,395

TIME: 12:46:41

Input Set: I004395.RAW

Does Not Comply
Corrected Diskette Needed

1 <110> Gilmore Jr., Robert D
2 Johnson, Barbara JB
3 <120> RECOMBINANT P37/FlaA AS A DIAGNOSTIC REAGENT
4 <130> 97,429
5 <140> US/09/004,395
6 <141> 1998-01-08
W--> 7 <150> *delete these numbers identify if*
8 <151>
E--> 9 <160> *#67 shown in file - do not put in P before*
10 <170> Microsoft Word 97

ERRORED SEQUENCES FOLLOW

Suggester Consult also
Seymour Rubin

E--> 11 <210> 1
12 <211> (1655) 1832 ntour (p 3)
13 <212> DNA
E--> 14 <213> ↑ move up - <220> does not have a response (it is a header only)
15 <220> (Unknown)
16 <221> CDS
17 <222> 473..1498 → insert (220) (see item 12 on Enve
18 <221> sig_peptide → summary
19 <222> 473..538 → insert (221) first)
20 <221> mat_peptide
21 <222> 539..1498
22 <223>
23 <400> 1
24 atgataatct tttttcaaaa aaggtttttt attttcattc tagcaaggga tttgttgcta 60
25 atttaagata tttaagagat gaacaaaatt tgaaagataa tttagatctt ttagtaaaaag 120
26 attttctttt aggaagcaat gagggggttt cttttggggt tttattaagt gattcaagat 180
27 ttttatattc ttttttaaag aatggagttt attatgtaaa tctttcaaga gaattttatg 240
28 attcttttaa taatggtgat tataatgaat cttttgatgt taagggtcaat ctttttgcta 300
29 tgtctttaat aaaaacaatg cgctttaact atcctggtta gataaaaaag attattatct 360

lys Arg Lys Ala Lys Ser Ile Leu Phe Phe Leu Leu Ser Thr Val Leu

-20 -15 -10

cct Pro	gga Gly	gaa Glu	tta Leu 15	gtc Val	tta Leu	gat Asp	ttt Phe	gcc Ala 20	gag Glu	ctt Leu	gca Ala	aga Arg	gat Asp 25	cca Pro	agt Ser	619
tca Ser	act Thr	aga Arg 30	ctt Leu	gat Asp	ctt Leu	aca Thr	aat Asn 35	tat Tyr	gtt Val	gat Asp	tat Tyr	gta Val 40	tat Tyr	tcg Ser	ggc Gly	667
gct Ala	tct Ser 45	ggt Gly	att Ile	gtt Val	aag Lys	ccg Pro 50	gaa Glu	gat Asp	atg Met	gtt Val	gta Val 55	gat Asp	ctt Leu	ggg Gly	ata Ile	715
aat Asn 60	aat Asn	tgg Trp	agc Ser	gtt Val	tta Leu 65	ctt Leu	act Thr	cct Pro	tct Ser	gca Ala 70	agg Arg	ttg Leu	cag Gln	gct Ala	tac Tyr 75	763
gtt Val	aaa Lys	aat Asn	tca Ser	gtt Val 80	gtt Val	gcg Ala	ccc Pro	gct Ala	gtt Val 85	gtt Val	aag Lys	agt Ser	gag Glu	tca Ser 90	aaa Lys	811
agg Arg	tac Tyr	gca Ala	ggt Gly 95	gat Asp	act Thr	att Ile	ttg Leu	ggg Gly 100	gta Val	aga Arg	gtt Val	ttg Leu	ttt Phe 105	cca Pro	agc Ser	859
tat Tyr	tct Ser	caa Gln 110	tca Ser	tct Ser	gct Ala	atg Met	att Ile 115	atg Met	cca Pro	cca Pro	ttt Phe	aaa Lys 120	att Ile	cct Pro	ttt Phe	907
tat Tyr	tca Ser 125	ggg Gly	gaa Glu	agt Ser	ggc Gly	aat Asn 130	caa Gln	ttt Phe	tta Leu	ggc Gly	aaa Lys 135	ggt Gly	ctt Leu	att Ile	gat Asp	955
aac Asn 140	att Ile	aaa Lys	acc Thr	atg Met	aaa Lys 145	gaa Glu	att Ile	aag Lys	gta Val	tct Ser 150	gtt Val	tat Tyr	agt Ser	tta Leu	ggg Gly 155	1003
tat Tyr	gag Glu	ata Ile	gat Asp	ctt Leu 160	gag Glu	gtt Val	tta Leu	ttt Phe	gaa Glu 165	gat Asp	atg Met	aat Asn	ggc Gly	atg Met 170	gaa Glu	1051
tat Tyr	gct Ala	tat Tyr	tct Ser 175	atg Met	ggt Gly	act Thr	tta Leu	aag Lys 180	ttt Phe	aaa Lys	ggg Gly	tgg Trp	gct Ala 185	gat Asp	tta Leu	1099
att Ile	tgg Trp	tca Ser 190	aat Asn	cct Pro	aac Asn	tat Tyr	att Ile 195	cct Pro	aat Asn	ata Ile	tca Ser	tcc Ser 200	aga Arg	att Ile	att Ile	1147

211 212 213 214 215 216 217 218 219 220 221 222 223 224 225
 Lys Ala Phe Arg Val Ser Lys Ser His Ser Ser Lys Val Lys Asn Phe
 220 225 230 235

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Ile Phe Tyr Val Lys Asp Leu Arg Val Leu Tyr Asp Lys Leu Ser Val
240 245 250

tca ata gat tct gat att gac agt gag tct gta ttt aaa gtt tat gag 1339
Ser Ile Asp Ser Asp Ile Asp Ser Glu Ser Val Phe Lys Val Tyr Glu
255 260 265

act agc gga act gaa tcc ctt cgt aaa tta aag gca cac gaa act ttt 1387
Thr Ser Gly Thr Glu Ser Leu Arg Lys Leu Lys Ala His Glu Thr Phe
270 275 280

aaa aga gtt tta aag ctt aga gaa aaa att tct atc gct gaa ggc tct 1435
Lys Arg Val Leu Lys Leu Arg Glu Lys Ile Ser Ile Ala Glu Gly Ser
285 290 295

ttc caa aac ttt gta gaa aag att gag agt gaa aaa cct gaa gaa tca 1483
Phe Gln Asn Phe Val Glu Lys Ile Glu Ser Glu Lys Pro Glu Glu Ser
300 305 310 315

tct ccg aaa aat tag gtttaaatta atatgtaaag ctacctaaaa ggtttgcttt 1538
Ser Pro Lys Asn *
320

acatattaaa ataataggaa atagtatatg gaaatattag atttggaaaa tgaagagctt 1598

ttaggagttt tttttgaaga agctcaaaat cttgtagata tccttgaaga gaatatt 1655

gcgcccgcaa tgtgagtttt tgtagttgga tttgctcccc cgccgtcgtt caatgagaat 60/715
ggataagagg ctgctgggat tgacgtgagg gggcagggat ggctataatt ctgggagcga 120/1775
actccgggagc aatatgaagc gcatcgatac aagttagttg tagggaggga accatgg 177/1832

<210> 2
<211> 342
<212> PRT → DNA
<213> Unknown → see item 12

<220>
<221>
<222>
<223>

<400> 2
ttgacgtgag ggggcaggga tggctatatt tctgggagcg aactccgggc gaata 55

<210> 3
<211> 55
<212> DNA
<213> Mustard

Leu Phe Ala Gln Glu Thr Asp Gly Leu Ala Glu Gly Ser Lys Arg Ala

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Glu	Pro	Gly	Glu	Leu	Val	Leu	Asp	Phe	Ala	Glu	Leu	Ala	Arg	Asp	Pro	
				15					20					25		
Ser	Ser	Thr	Arg	Leu	Asp	Leu	Thr	Asn	Tyr	Val	Asp	Tyr	Val	Tyr	Ser	
			30					35					40			
Gly	Ala	Ser	Gly	Ile	Val	Lys	Pro	Glu	Asp	Met	Val	Val	Asp	Leu	Gly	
		45					50					55				
Ile	Asn	Asn	Trp	Ser	Val	Leu	Leu	Thr	Pro	Ser	Ala	Arg	Leu	Gln	Ala	
	60					65					70					
Tyr	Val	Lys	Asn	Ser	Val	Val	Ala	Pro	Ala	Val	Val	Lys	Ser	Glu	Ser	
75					80					85				90		
Lys	Arg	Tyr	Ala	Gly	Asp	Thr	Ile	Leu	Gly	Val	Arg	Val	Leu	Phe	Pro	
				95					100					105		
Ser	Tyr	Ser	Gln	Ser	Ser	Ala	Met	Ile	Met	Pro	Pro	Phe	Lys	Ile	Pro	
			110					115					120			
Phe	Tyr	Ser	Gly	Glu	Ser	Gly	Asn	Gln	Phe	Leu	Gly	Lys	Gly	Leu	Ile	
		125					130					135				
Asp	Asn	Ile	Lys	Thr	Met	Lys	Glu	Ile	Lys	Val	Ser	Val	Tyr	Ser	Leu	
	140					145					150					
Gly	Tyr	Glu	Ile	Asp	Leu	Glu	Val	Leu	Phe	Glu	Asp	Met	Asn	Gly	Met	
155					160					165					170	
Glu	Tyr	Ala	Tyr	Ser	Met	Gly	Thr	Leu	Lys	Phe	Lys	Gly	Trp	Ala	Asp	
				175					180					185		
Leu	Ile	Trp	Ser	Asn	Pro	Asn	Tyr	Ile	Pro	Asn	Ile	Ser	Ser	Arg	Ile	
			190					195					200			
Ile	Lys	Asp	Asp	Val	Pro	Asn	Tyr	Pro	Leu	Ala	Ser	Ser	Lys	Met	Arg	
		205					210					215				
Phe	Lys	Ala	Phe	Arg	Val	Ser	Lys	Ser	His	Ser	Ser	Lys	Val	Lys	Asn	
	220					225					230					
Phe	Ile	Phe	Tyr	Val	Lys	Asp	Leu	Arg	Val	Leu	Tyr	Asp	Lys	Leu	Ser	
235					240					245					250	
Val	Ser	Ile	Asp	Ser	Asp	Ile	Asp	Ser	Glu	Ser	Val	Phe	Lys	Val	Tyr	
				255					260					265		

Ser Phe Gln Asn Phe Val Glu Lys Ile Glu Ser Glu Lys Pro Glu Glu

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Ser Ser Pro Lys Asn
315

(*)
820 delete

<210> 3

<211> 21

<212> DNA

<213> Unknown

item 12

Another sequence 3?

<400> 3

atgaaaagga aagctaaaag t

21

<210> 4

<211> 19

<212> DNA

<213> Unknown

item 12

<400> 4

gatggattag cagaggggtt

19

<210> 5

<211> 21

<212> DNA

<213> Unknown

item 12

<400> 5

tgggataaat aattggagcg t

21

<210> 6

<211> 21

<212> DNA

<213> Unknown

item 12

<400> 6

ctaatttttc ggagatgatt c

21

(1) delete